RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/771,833
Source: EFW
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RAW SEQUENCE LISTING DATE: 10/29/2004
PATENT APPLICATION: **US/10/771,833** TIME: 11:12:12

Input Set : **A:\39363106.app**
Output Set: **N:\CRF4\10292004\J771833.raw**

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 3 <110> APPLICANT: MILBURN, MICHAEL V.
 5 <120> TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
 7 <130> FILE REFERENCE: 039363-1106
 9 <140> CURRENT APPLICATION NUMBER: 10/771,833
10 <141> CURRENT FILING DATE: 2004-02-03
12 <150> PRIOR APPLICATION NUMBER: 60/485,627
13 <151> PRIOR FILING DATE: 2003-07-07
15 <150> PRIOR APPLICATION NUMBER: 60/444,734
16 <151> PRIOR FILING DATE: 2003-02-03
18 <160> NUMBER OF SEQ ID NOS: 31
20 <170> SOFTWARE: PatentIn Ver. 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 875
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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32              20                  25                  30
34 Trp Leu Asp Asp His Trp Asp Phe Thr Phe Ser Tyr Phe Val Arg Lys
35          35                  40                  45
37 Ala Thr Arg Glu Met Val Asn Ala Trp Phe Ala Glu Arg Val His Thr
38      50                  55                  60
40 Ile Pro Val Cys Lys Glu Gly Ile Arg Gly His Thr Glu Ser Cys Ser
41  65                  70                  75                  80
43 Cys Pro Leu Gln Gln Ser Pro Arg Ala Asp Asn Ser Val Pro Gly Thr
44                  85                  90                  95
46 Pro Thr Arg Lys Ile Ser Ala Ser Glu Phe Asp Arg Pro Leu Arg Pro
47              100                 105                 110
49 Ile Val Val Lys Asp Ser Glu Gly Thr Val Ser Phe Leu Ser Asp Ser
50          115                 120                 125
52 Glu Lys Lys Glu Gln Met Pro Leu Thr Pro Pro Arg Phe Asp His Asp
53      130                 135                 140
55 Glu Gly Asp Gln Cys Ser Arg Leu Leu Glu Leu Val Lys Asp Ile Ser
56 145                 150                 155                 160
58 Ser His Leu Asp Val Thr Ala Leu Cys His Lys Ile Phe Leu His Ile
59                  165                 170                 175
61 His Gly Leu Ile Ser Ala Asp Arg Tyr Ser Leu Phe Leu Val Cys Glu
62              180                 185                 190
64 Asp Ser Ser Asn Asp Lys Phe Leu Ile Ser Arg Leu Phe Asp Val Ala
65          195                 200                 205
67 Glu Gly Ser Thr Leu Glu Glu Val Ser Asn Asn Cys Ile Arg Leu Glu
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68     210                 215                 220
70 Trp Asn Lys Gly Ile Val Gly His Val Ala Ala Leu Gly Glu Pro Leu
71 225                 230                 235                 240
73 Asn Ile Lys Asp Ala Tyr Glu Asp Pro Arg Phe Asn Ala Glu Val Asp
74                 245                 250                 255
76 Gln Ile Thr Gly Tyr Lys Thr Gln Ser Ile Leu Cys Met Pro Ile Lys
77             260                 265                 270
79 Asn His Arg Glu Glu Val Val Gly Val Ala Gln Ala Ile Asn Lys Lys
80         275                 280                 285
82 Ser Gly Asn Gly Gly Thr Phe Thr Glu Lys Asp Glu Lys Asp Phe Ala
83     290                 295                 300
85 Ala Tyr Leu Ala Phe Cys Gly Ile Val Leu His Asn Ala Gln Leu Tyr
86 305                 310                 315                 320
88 Glu Thr Ser Leu Leu Glu Asn Lys Arg Asn Gln Val Leu Leu Asp Leu
89                 325                 330                 335
91 Ala Ser Leu Ile Phe Glu Glu Gln Gln Ser Leu Glu Val Ile Leu Lys
92             340                 345                 350
94 Lys Ile Ala Ala Thr Ile Ile Ser Phe Met Gln Val Gln Lys Cys Thr
95         355                 360                 365
97 Ile Phe Ile Val Asp Glu Asp Cys Ser Asp Ser Phe Ser Ser Val Phe
98     370                 375                 380
100 His Met Glu Cys Glu Glu Leu Glu Lys Ser Ser Asp Thr Leu Thr Arg
101 385                 390                 395                 400
103 Glu His Asp Ala Asn Lys Ile Asn Tyr Met Tyr Ala Gln Tyr Val Lys
104                 405                 410                 415
106 Asn Thr Met Glu Pro Leu Asn Ile Pro Asp Val Ser Lys Asp Lys Arg
107             420                 425                 430
109 Phe Pro Trp Thr Thr Glu Asn Thr Gly Asn Val Asn Gln Gln Cys Ile
110         435                 440                 445
112 Arg Ser Leu Leu Cys Thr Pro Ile Lys Asn Gly Lys Lys Asn Lys Val
113     450                 455                 460
115 Ile Gly Val Cys Gln Leu Val Asn Lys Met Glu Glu Asn Thr Gly Lys
116 465                 470                 475                 480
118 Val Lys Pro Phe Asn Arg Asn Asp Glu Gln Phe Leu Glu Ala Phe Val
119                 485                 490                 495
121 Ile Phe Cys Gly Leu Gly Ile Gln Asn Thr Gln Met Tyr Glu Ala Val
122             500                 505                 510
124 Glu Arg Ala Met Ala Lys Gln Met Val Thr Leu Glu Val Leu Ser Tyr
125         515                 520                 525
127 His Ala Ser Ala Ala Glu Glu Glu Thr Arg Glu Leu Gln Ser Leu Ala
128     530                 535                 540
130 Ala Ala Val Val Pro Ser Ala Gln Thr Leu Lys Ile Thr Asp Phe Ser
131 545                 550                 555                 560
133 Phe Ser Asp Phe Glu Leu Ser Asp Leu Glu Thr Ala Leu Cys Thr Ile
134                 565                 570                 575
136 Arg Met Phe Thr Asp Leu Asn Leu Val Gln Asn Phe Gln Met Lys His
137             580                 585                 590
139 Glu Val Leu Cys Arg Trp Ile Leu Ser Val Lys Lys Asn Tyr Arg Lys
140         595                 600                 605
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142 Asn Val Ala Tyr His Asn Trp Arg His Ala Phe Asn Thr Ala Gln Cys
143     610                 615                 620
145 Met Phe Ala Ala Leu Lys Ala Gly Lys Ile Gln Asn Lys Leu Thr Asp
146 625                 630                 635                 640
148 Leu Glu Ile Leu Ala Leu Leu Ile Ala Ala Leu Ser His Asp Leu Asp
149                 645                 650                 655
151 His Arg Gly Val Asn Asn Ser Tyr Ile Gln Arg Ser Glu His Pro Leu
152             660                 665                 670
154 Ala Gln Leu Tyr Cys His Ser Ile Met Glu His His His Phe Asp Gln
155         675                 680                 685
157 Cys Leu Met Ile Leu Asn Ser Pro Gly Asn Gln Ile Leu Ser Gly Leu
158     690                 695                 700
160 Ser Ile Glu Glu Tyr Lys Thr Thr Leu Lys Ile Ile Lys Gln Ala Ile
161 705                 710                 715                 720
163 Leu Ala Thr Asp Leu Ala Leu Tyr Ile Lys Arg Arg Gly Glu Phe Phe
164                 725                 730                 735
166 Glu Leu Ile Arg Lys Asn Gln Phe Asn Leu Glu Asp Pro His Gln Lys
167             740                 745                 750
169 Glu Leu Phe Leu Ala Met Leu Met Thr Ala Cys Asp Leu Ser Ala Ile
170         755                 760                 765
172 Thr Lys Pro Trp Pro Ile Gln Gln Arg Ile Ala Glu Leu Val Ala Thr
173     770                 775                 780
175 Glu Phe Phe Asp Gln Gly Asp Arg Glu Arg Lys Glu Leu Asn Ile Glu
176 785                 790                 795                 800
178 Pro Thr Asp Leu Met Asn Arg Glu Lys Lys Asn Lys Ile Pro Ser Met
179                 805                 810                 815
181 Gln Val Gly Phe Ile Asp Ala Ile Cys Leu Gln Leu Tyr Glu Ala Leu
182             820                 825                 830
184 Thr His Val Ser Glu Asp Cys Phe Pro Leu Leu Asp Gly Cys Arg Lys
185         835                 840                 845
187 Asn Arg Gln Lys Trp Gln Ala Leu Ala Glu Gln Gln Glu Lys Met Leu
188     850                 855                 860
190 Ile Asn Gly Glu Ser Gly Gln Ala Lys Arg Asn
191 865                 870                 875
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 3106
196 <212> TYPE: DNA
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 2
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201 gggtctcgag gccgagtcct gttcttctga gggacggacc ccagctgggg tggaaaagca 120
202 gtaccagaga gcctccgagg cgcgcggtgc caaccatgga gcgggccggc cccagcttcg 180
203 ggcagcagcg acagcagcag cagccccagc agcagaagca gcagcagagg gatcaggact 240
204 cggtcgaagc atggctggac gatcactggg actttacctt ctcatacttt gttagaaaag 300
205 ccaccagaga aatggtcaat gcatggtttg ctgagagagt tcacaccatc cctgtgtgca 360
206 aggaaggtat cagaggccac accgaatctt gctcttgtcc cttgcagcag agtcctcgtg 420
207 cagataacag tgtccctgga acaccaacca ggaaaatctc tgcctctgaa tttgaccggc 480
208 ctcttagacc cattgttgtc aaggattctg agggaactgt gagcttcctc tctgactcag 540
209 aaaagaagga acagatgcct ctaacccctc caaggtttga tcatgatgaa ggggaccagt 600
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210 gctcaagact cttggaatta gtgaaggata tttctagtca tttggatgtc acagccttat 660
211 gtcacaaaat tttcttgcat atccatggac tgatatctgc tgaccgctat tccctgttcc 720
212 ttgtctgtga agacagctcc aatgacaagt ttcttatcag ccgcctcttt gatgttgctg 780
213 aaggttcaac actggaagaa gtttcaaata actgtatccg cttagaatgg aacaaaggca 840
214 ttgtgggaca tgtggcagcg cttggtgagc ccttgaacat caaagatgca tatgaggatc 900
215 ctcggttcaa tgcagaagtt gaccaaatta caggctacaa gacacaaagc attctttgta 960
216 tgccaattaa gaatcatagg gaagaggttg ttggtgtagc ccaggccatc aacaagaaat 1020
217 caggaaacgg tgggacattt actgaaaaag atgaaaagga ctttgctgct tatttggcat 1080
218 tttgtggtat tgttcttcat aatgctcagc tctatgagac ttcactgctg gagaacaaga 1140
219 gaaatcaggt gctgcttgac cttgctagtt taatttttga agaacaacaa tcattagaag 1200
220 taattttgaa gaaaatagct gccactatta tctctttcat gcaagtgcag aaatgcacca 1260
221 ttttcatagt ggatgaagat tgctccgatt ctttttctag tgtgtttcac atggagtgtg 1320
222 aggaattaga aaaatcatct gatacattaa caagggaaca tgatgcaaac aaaatcaatt 1380
223 acatgtatgc tcagtatgtc aaaaatacta tggaaccact taatatccca gatgtcagta 1440
224 aggataaaag atttccctgg acaactgaaa atacaggaaa tgtaaaccag cagtgcatta 1500
225 gaagtttgct ttgtacacct ataaaaaatg gaaagaagaa taaagttata ggggtttgcc 1560
226 aacttgttaa taagatggag gagaatactg gcaaggttaa gcctttcaac cgaaatgacg 1620
227 aacagtttct ggaagctttt gtcatctttt gtggcttggg gatccagaac acgcagatgt 1680
228 atgaagcagt ggagagagcc atggccaagc aaatggtcac attggaggtt ctgtcgtatc 1740
229 atgcttcagc agcagaggaa gaaacaagag agctacagtc gttagcggct gctgtggtgc 1800
230 catctgccca gacccttaaa attactgact ttagcttcag tgactttgag ctgtctgatc 1860
231 tggaaacagc actgtgtaca attcggatgt ttactgacct caaccttgtg cagaacttcc 1920
232 agatgaaaca tgaggttctt tgcagatgga ttttaagtgt taagaagaat tatcggaaga 1980
233 atgttgccta tcataattgg agacatgcct ttaatacagc tcagtgcatg tttgctgctc 2040
234 taaaagcagg caaaattcag aacaagctga ctgacctgga gatacttgca ttgctgattg 2100
235 ctgcactaag ccacgatttg gatcaccgtg gtgtgaataa ctcttacata cagcgaagtg 2160
236 aacatccact tgcccagctt tactgccatt caatcatgga acaccatcat tttgaccagt 2220
237 gcctgatgat tcttaatagt ccaggcaatc agattctcag tggcctctcc attgaagaat 2280
238 ataagaccac gttgaaaata atcaagcaag ctattttagc tacagaccta gcactgtaca 2340
239 ttaagaggcg aggagaattt tttgaactta taagaaaaaa tcaattcaat ttggaagatc 2400
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241 caaaaccctg gcctattcaa caacggatag cagaacttgt agcaactgaa ttttttgatc 2520
242 aaggagacag agagagaaaa gaactcaaca tagaacccac tgatctaatg aacagggaga 2580
243 agaaaaacaa aatcccaagt atgcaagttg ggttcataga tgccatctgc ttgcaactgt 2640
244 atgaggccct gacccacgtg tcagaggact gtttcccttt gctagatggc tgcagaaaga 2700
245 acaggcagaa atggcaggcc cttgcagaac agcaggagaa gatgctgatt aatggggaaa 2760
246 gcggccaggc caagcggaac tgagtggcct atttcatgca gagttgaagt ttacagagat 2820
247 ggtgtgttct gcaatatgcc tagtttctta cacactgtct gtatagtgtc tgtatttggt 2880
248 atatactttg ccactgctgt atttttattt ttgcacaact tttgagagta tagcatgaat 2940
249 gtttttagag gactattaca tatttttttgt atatttgttt tatgctactg aactgaaagg 3000
250 atcaacaaca tccactgtta gcacattgat aaaagcattg tttgtgatat ttcgtgtact 3060
251 gcaaagtgta tgcagtattc ttgcactgag gttttttttgc ttgggg 3106
254 <210> SEQ ID NO: 3
255 <211> LENGTH: 33
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
262 <400> SEQUENCE: 3

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263 gtcgtatcat atgtcagcag cagaggaaga aac                                    33
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 32
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
274 <400> SEQUENCE: 4
275 tctgcagtcg acaggccact cagttccgct tg                                    32
278 <210> SEQ ID NO: 5
279 <211> LENGTH: 391
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Pet15S construct
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (108)..(170)
290 <400> SEQUENCE: 5
291 agatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 60
293 ttcccctcta gaaataattt tgtttaactt taagaaggag atatacc atg ggc agc   116
294                                                    Met Gly Ser
295                                                      1
297 agc cat cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc   164
298 Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
299       5                  10                  15
301 cat atg ggatccggaa ttcaaaggcc tacgtcgact agagcctgca gtctcgacca    220
302 His Met
303  20
305 tcatcatcat catcattaat aaaagggcga attccagcac actggcggcc gttactagtg 280
307 gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa 340
309 taactagcat aacccccttgg ggcctctaaa cgggtcttga ggggtttttt g          391
312 <210> SEQ ID NO: 6
313 <211> LENGTH: 21
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: Pet15S construct
320 <400> SEQUENCE: 6
321 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
322   1               5                  10                  15
324 Arg Gly Ser His Met
325              20
329 <210> SEQ ID NO: 7
330 <211> LENGTH: 6
331 <212> TYPE: PRT
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Description of Artificial Sequence: 6-His tag
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VERIFICATION SUMMARY DATE: 10/29/2004
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